NCBI   results of BLAST

BLASTN 2.2.6 [Apr-09-2003]

RID: 1064960959-20664-530139.BLASTQ3
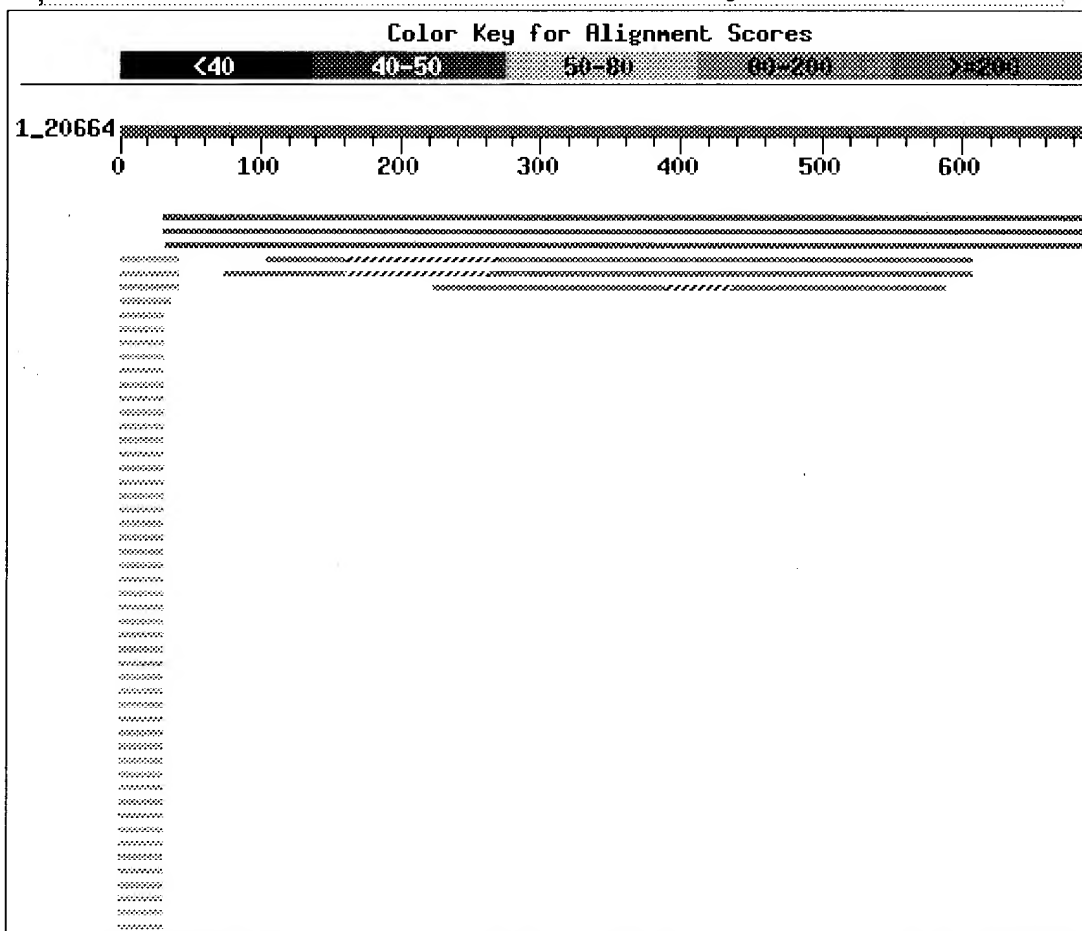
Query= .
       (689 letters)

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, or phase 0, 1 or 2 HTGS sequences)
       1,931,681 sequences; 9,156,315,655 total letters

Taxonomy reports

Distribution of 106 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments

Color Key for Alignment Scores				
<40	40-50	50-80	80-200	>=200

Sequences producing significant alignments: Score   E
                                            (bits) Value

gi|505280|emb|X59040.1|CBDPEXC3   Clostridium botulinum D pha...   1261   0.0
gi|296786|emb|X59039.1|CBCPEXC3   Clostridium botulinum C pha...   1261   0.0
gi|14907|emb|X51464.1|CBDPE3   Clostridium botulinum D Phage ...   1257   0.0
gi|144736|gb|M74038.1|CLOC3ADP   C.botulinum C3 ADP-ribosyltr...   184   1e-43
gi|404820|dbj|D17555.1|CLOADPRC3   Clostridium botulinum type...   172   5e-40
gi|1212874|emb|X87215.1|CLC3GENE   C.limosum C3 gene   100   6e-18
gi|33149672|gb|AY330212.1| Cloning vector pT3, complete seq...   68   2e-08
gi|595779|gb|U13871.1|XXU13871   pT7T3D cloning vector, compl...   68   2e-08
gi|595774|gb|U13869.1|XXU13869   pT7T318U cloning vector, com...   68   2e-08
gi|1149706|emb|X86491.1|CPSPOOA   C.perfringens spoOA gene   66   9e-08
gi|31335236|gb|AY292466.1| BAC cloning vector pBACVM4, comp...   64   3e-07
gi|30424554|gb|AY182782.1| Shuttle vector pSK5640, complete...   64   3e-07
gi|30424549|gb|AY182781.1| Shuttle vector pSK5632, complete...   64   3e-07
gi|29838547|gb|AY265466.1| Shuttle vector pAM2770, complete...   64   3e-07
gi|29825787|gb|AY263154.1| Cloning vector pAM2600, complete...   64   3e-07
gi|29415162|gb|AY150268.1| CRIM plasmid pSK67, complete seq...   64   3e-07
gi|29373934|gb|AY219701.1| Cloning vector pAZ1, complete se...   64   3e-07
gi|22595311|gb|AF405697.1| Reporter vector pALH122, complet...   64   3e-07
gi|28207668|gb|AY187276.1| Shuttle vector pBSV2, complete s...   64   3e-07
gi|21952452|gb|AF524829.1| P-element cloning system vector ...   64   3e-07
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gi|21730275|gb|AF521666.1| Cloning vector pLOI2065 complete...   64   3e-07
gi|25141017|gb|AC116033.2| Zea mays genomic clone ZM15C05 ...   64   3e-07
gi|22074797|gb|AY112734.1| Broad host range vector pMLS7, c...   64   3e-07
gi|22074788|gb|AY112733.1| Broad host range vector pMLBAD, ...   64   3e-07
gi|5824688|emb|AL110477.1|CEY113G7B   Caenorhabditis elegans ...   64   3e-07
gi|34556140|emb|BX005348.8| Zebrafish DNA sequence from clo...   64   3e-07
gi|33457134|emb|AJ560658.1|SSC560658   Sus scrofa partial mRN...   64   3e-07
gi|4567137|gb|AF134471.1| Homo sapiens chromosome 10 clone ...   64   3e-07
gi|21617574|gb|AF519766.1| Cloning vector pMAK705, complete...   64   3e-07
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gi|11559661|gb|AF294978.1| Cloning vector pC1300intC, compl...   64   3e-07
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gi|20455693|gb|AC110750.4| Homo sapiens chromosome 17, clon...   64   3e-07
gi|5419758|emb|AJ246004.1|HSA246004   Homo sapiens RET gene, ...   64   3e-07
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gi|18654300|gb|L47837.1|SYNKIL199P   Cloning vector pKIL199 c...   64   3e-07
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gi|14794547|gb|AF327711.1|AF327711   Cloning vector pDN19, co...   64   3e-07
gi|18041969|gb|AF337031.1|AF337031   Aphidius ervi clone 110 ...   64   3e-07
gi|18041957|gb|AF337016.1|AF337016   Aphidius ervi clone 34 m...   64   3e-07
gi|18041950|gb|AF337003.1|AF337003   Aphidius ervi clone 13R ...   64   3e-07
gi|18041946|gb|AF336997.1|AF336997   Aphidius ervi clone 107 ...   64   3e-07
gi|18041941|gb|AF336992.1|AF336992   Aphidius ervi clone 47 m...   64   3e-07
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gi|13345295|gb|AF323603.1|AF323603   Cloning vector pPOP, com...   64   3e-07
gi|8308058|gb|AF261959.1|AF261959   Anourosorex squamipes clo...   64   3e-07
gi|9294791|gb|AF178451.1|AF178451   Integration vector pCD11P...   64   3e-07
gi|8927566|gb|AF276982.1|AF276982   Integrative vector pNLE1,...   64   3e-07

gi|8650401|gb|AF216802.1|AF216802	Shuttle vector pDL278, co...	64	3e-07
gi|8272485|gb|AF219942.1|AF219942	Shuttle vector pPha-T1 co...	64	3e-07
gi|7715975|gb|AF203972.1|AF203972	Shuttle vector pBA comple...	64	3e-07
gi|7705080|gb|AC068564.1|AC068564	Filobasidiella neoformans...	64	3e-07
gi|5689998|emb|AJ131112.1|SSC131112	Sus scrofa MHC class I ...	64	3e-07
gi|28300623|emb|AL953891.10|	Zebrafish DNA sequence from cl...	64	3e-07
gi|7638149|gb|AF234316.1|AF234316	Binary vector pCAMBIA-230...	64	3e-07
gi|7638145|gb|AF234315.1|AF234315	Binary vector pCAMBIA-230...	64	3e-07
gi|7638140|gb|AF234314.1|AF234314	Binary vector pCAMBIA-220...	64	3e-07
gi|7638136|gb|AF234313.1|AF234313	Binary vector pCAMBIA-220...	64	3e-07
gi|7638083|gb|AF234300.1|AF234300	Binary vector pCAMBIA-130...	64	3e-07
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gi|27531019|dbj|AB082961.1|	Cloning vector pMG171 DNA, comp...	64	3e-07
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gi|4731621|gb|AF134572.1|AF134572	Cloning vector p34S-Sm2, ...	64	3e-07
gi|3907623|gb|AF102233.1|AF102233	Transposon delivery vecto...	64	3e-07
gi|3136321|gb|AF064067.1|AF064067	Expression vector pYZ81N,...	64	3e-07
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gi|29164973|gb|AY219694.1|	Shuttle vector pBHK18mob2, compl...	64	3e-07
gi|29164970|gb|AY219693.1|	Shuttle vector pBHC18mob2, compl...	64	3e-07
gi|29164967|gb|AY219692.1|	Shuttle vector pBHT18, complete ...	64	3e-07
gi|29164964|gb|AY219691.1|	Shuttle vector pBHK18, complete ...	64	3e-07
gi|29164961|gb|AY219690.1|	Shuttle vector pBHC18, complete ...	64	3e-07
gi|29164958|gb|AY219689.1|	Expression vector pXT99A, comple...	64	3e-07
gi|29164955|gb|AY219688.1|	Expression vector pXS99A, comple...	64	3e-07
gi|29164951|gb|AY219687.1|	Expression vector pXK99CAT, comp...	64	3e-07
gi|4827116|dbj|AP000150.1|	Homo sapiens genomic DNA, chromo...	64	3e-07
gi|6468567|emb|AJ131034.1|HSA131034	Homo sapiens otase gene...	58	2e-05

Alignments

Get selected sequences | Select all | Deselect all

☐ >gi\|505280\|emb\|X59040.1\|CBDPEXC3   Clostridium botulinum D phage gene for exoenzym
          Length = 1979

Score = 1261 bits (636), Expect = 0.0
Identities = 654/659 (99%), Gaps = 1/659 (0%)
Strand = Plus / Plus

Query: 32   atgcttattccattaatcaaa-ggcttattcaaatacttaccaggagtttactaatattg 90
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Sbjct:  883   atcaagcaaaagcttggggtaatgctcagtataaaaagtatggactaagcaaatcagaaa  942


Query:  151   aagaagctatagtatcatatactaaaagcgctagtgaaataaatggaaagctaagacaaa  210
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Sbjct:  943   aagaagctatagtatcatatactaaaagcgctagtgaaataaatggaaagctaagacaaa  1002


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Query:  271   aatcttttaataaaatgaagacccctgaaaatattatgttatttagaggcgacgaccctg  330
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Query:  331   cttatttaggaacagaatttcaaaacactcttcttaattcaaatggtacaattaataaaa  390
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Sbjct: 1123   cttatttaggaacagaatttcaaaacactcttcttaattcaaatggtacaattaataaaa  1182


Query:  391   cggcttttgaaaaggctaaagctaagtttttaaataaagatagacttgaatatggatata  450
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1183   cggcttttgaaaaggctaaagctaagtttttaaataaagatagacttgaatatggatata  1242


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Query:  511   aagtagcaaaaggctcaaaggcaggatatattgaccctattagtgcttttcagggacaac  570
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☐ >gi|296786|emb|X59039.1|CBCPEXC3   Clostridium botulinum C phage gene for exoenzym
              Length = 1977

 Score = 1261 bits (636), Expect = 0.0
 Identities = 654/659 (99%), Gaps = 1/659 (0%)
 Strand = Plus / Plus

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Query: 91    atcaagcaaaagcttggggtaatgctcagtataaaaagtatggactaagcaaatcagaaa 150
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Sbjct: 881   atcaagcaaaagcttggggtaatgctcagtataaaaagtatggactaagcaaatcagaaa 940


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
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 Strand = Plus / Plus


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Query: 93   caagcaaaagcttggggtaatgctcagtataaaaagtatggactaagcaaatcagaaaaa 152
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Query: 153  gaagctatagtatcatatactaaaagcgctagtgaaataaatggaaagctaagacaaaat 212
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 121  gaagctatagtatcatatactaaaagcgctagtgaaataaatggaaagctaagacaaaat 180


Query: 213  aagggagttatcaatggatttccttcaaatttaataaaacaagttgaacttttagataaa 272
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Sbjct: 181  aagggagttatcaatggatttccttcaaatttaataaaacaagttgaacttttagataaa 240


Query: 273  tcttttaataaaatgaagacccctgaaaatattatgttatttagaggcgacgaccctgct 332
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Sbjct: 241  tcttttaataaaatgaagacccctgaaaatattatgttatttagaggcgacgaccctgct 300


Query: 333  tatttaggaacagaatttcaaaacactcttcttaattcaaatggtacaattaataaaacg 392
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 301  tatttaggaacagaatttcaaaacactcttcttaattcaaatggtacaattaataaaacg 360


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Query: 513  gtagcaaaaggctcaaaggcaggatatattgaccctattagtgcttttcagggacaactt 572
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Sbjct: 481  gtagcaaaaggctcaaaggcaggatatattgaccctattagtgcttttgcaggacaactt 540


Query: 573  gaaatgttgcttcctagacatagtacttatcatatagacgatatgagattgtcttctgat 632
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Sbjct: 541  gaaatgttgcttcctagacatagtacttatcatatagacgatatgagattgtcttctgat 600


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 Score = 184 bits (93), Expect = 1e-43
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 Strand = Plus / Plus

Query: 271   aatcttttaataaaatgaagacccctgaaaatattatgttatttagaggcgacgaccctg 330
              ||||||||| ||| ||||||| ||| |||||||||| | |||||||| || |||||||
Sbjct: 772   aatcttttagtaagatgaagatgcctcaaaatattattctttttagaggtgatgaccctg 831

Query: 331   cttatttaggaacagaatttcaaaacactcttcttaattcaaatggtacaattaataaaa 390
              |||||||||| |||||||||||| | | |||||||| | |||| |||||||||||||
Sbjct: 832   cttatttaggtccagaatttcaagataaaattcttaataaagatggaacaattaataaaa 891

Query: 391   cggcttttgaaaaggctaaagctaagttttaaataaagatagacttgaatatggatata 450
              | | ||||||| | | ||||||| || |||||||| || |||||| ||||||||||||
Sbjct: 892   ctgtttttgaacaagttaaagcgaaatttttaaaaaaggatagaacagaatatggatata 951

Query: 451   ttagtacttcattaatgaatgtttctcaatttgcaggaagaccaattattacanaattta 510
              ||||||||||||||||||| || | ||||||| ||||||||||||| |||| ||||||
Sbjct: 952   ttagtacttcattaatgagtg---cgcaatttggaggaagaccaattgttactaaattta 1008

Query: 511   aagtagcaaaaggctcaaaggcaggatatattgaccctattagtgcttttcagggacaac 570
              ||||| | || || ||||| | ||| ||||| ||||||||||| ||| | |||||||
Sbjct: 1009   aagtaactaatggatcaaaaggagggtatatagaccctattagctatttcccaggacaac 1068

Query: 571   ttgaaatgttgcttcctagacatagtacttatcatata 608
              ||||| |||||||||||||| ||| || |||| |||||
Sbjct: 1069   ttgaagtgttgcttcctagaaataatagttattatata 1106

  Score = 58.0 bits (29), Expect = 2e-05
  Identities = 50/57 (87%)
  Strand = Plus / Plus

Query: 105   tggggtaatgctcagtataaaaagtatggactaagcaaatcagaaaaagaagctata 161
              ||||| ||||||||| ||||||| ||||||| ||||| ||||||||| | ||| |||||||||||
Sbjct: 606   tggggaaatgctcaatataaaaaatatggcctaagcaaacctgaacaagaagctata 662

>gi|404820|dbj|D17555.1|CLOADPRC3   Clostridium botulinum type D gene for ADP-ribo
              complete cds
          Length = 1712

 Score = 172 bits (87), Expect = 5e-40
 Identities = 280/344 (81%), Gaps = 3/344 (0%)
 Strand = Plus / Plus

```
Query: 265  tagataaatcttttaataaaatgaagacccctgaaaatattatgttatttagaggcgacg 324
            |||||  ||||||||| |||  |||||||  |||  |||||||||| | |||||||| || |
Sbjct: 764  tagatcaatcttttagtaagatgaagatgcctcaaaatattattctttttagaggtgatg 823


Query: 325  accctgcttatttaggaacagaatttcaaaacactcttcttaattcaaatggtacaatta 384
            |||||||||||||||||| ||||||||||| | |    ||||||||| | |||| |||||||
Sbjct: 824  accctgcttatttaggtccagaatttcaagataaaattcttaataaagatggaacaatta 883


Query: 385  ataaaacggcttttgaaaaggctaaagctaagtttttaaataaagatagacttgaatatg 444
            ||| |   | ||||||| | | ||||||| || |||||||| |||||||||   |||||||
Sbjct: 884  atagagatgtttttgaacaagttaaagcgaaattttttaaaaaaagatagaacagaatatg 943


Query: 445  gatatattagtacttcattaatgaatgtttctcaatttgcaggaagaccaattattacan 504
            ||||||||||||||||||||||||||| ||     | ||||||| ||||||||||| ||||
Sbjct: 944  gatatattagtacttcattaatgagtg---cgcaatttggaggaagaccaattgttacta 1000


Query: 505  aatttaaagtagcaaaaggctcaaaggcaggatatattgaccctattagtgcttttcagg 564
            |||||||||||| | || || ||||| | ||| ||||| |||||||||||||||   ||| | |
Sbjct: 1001 aatttaaagtaactaatggatcaaaaggagggtatatagaccctattagctatttcccag 1060


Query: 565  gacaacttgaaatgttgcttcctagacatagtacttatcatata 608
            ||||||||||| |||||||||||||||| ||| || |||| |||||
Sbjct: 1061 gacaacttgaagtgttgcttcctagaaataatagttattatata 1104
```

 Score = 61.9 bits (31), Expect = 1e-06
 Identities = 73/87 (83%)
 Strand = Plus / Plus

```
Query: 75   gagtttactaatattgatcaagcaaaagcttggggtaatgctcagtataaaaagtatgga 134
            |||||||||||| ||||  ||||  ||| |||   ||||| |||||||| |||||||| |||||
Sbjct: 574  gagtttactaatgttgaggaagccaaaaaatggggaaatgctcaatataaaaaatatggc 633


Query: 135  ctaagcaaatcagaaaaagaagctata 161
            ||||||||| |  ||| |||||||||||
Sbjct: 634  ctaagcaaacctgaacaagaagctata 660
```


 >gi|1212874|emb|X87215.1|CLC3GENE   C.limosum C3 gene
          Length = 1022

 Score = 99.6 bits (50), Expect = 6e-18
 Identities = 127/153 (83%)
 Strand = Plus / Plus


```
Query: 438  gaatatggatatattagtacttcattaatgaatgtttctcaatttgcaggaagaccaatt 497
            ||||||||||||||||||| ||||| ||| | |||| |||   |.||||||| |||||||||
Sbjct: 673  gaatatggatatattagcacttctttagtaaatggttcagcatttgcaggtagaccaatt 732
```

```
Query: 498 attacanaatttaaagtagcaaaaggctcaaaggcaggatatattgaccctattagtgct 557
            ||  |||  |||||||  ||     |  |  ||  |||||  ||||||||||||||  ||||||||||  |
Sbjct: 733 ataacaaaatttaaggttttagacggttcaaaagcaggatatattgaacctattagtacc 792


Query: 558 tttcagggacaacttgaaatgttgcttcctaga 590
            |||  |  ||  |||||||||||  |||||||||||||
Sbjct: 793 tttaaaggtcaacttgaagtgttgcttcctaga 825



 Score = 75.8 bits (38), Expect = 9e-11
 Identities = 134/166 (80%)
 Strand = Plus / Plus


Query: 224 caatggatttccttcaaatttaataaaacaagttgaacttttagataaatcttttaataa 283
            ||||||||||  |||  ||  ||  |||  ||||  ||||||||||||     |||||||||||||  |  |||
Sbjct: 459 caatggattacctgcagatataagaaaagaagttgaacaaatagataaatctttcactaa 518


Query: 284 aatgaagacccctgaaaatattatgttatttagaggcgacgaccctgcttatttaggaac 343
            ||||  |  ||  ||||||||||||||||||   |  |||||||||  ||  ||  ||||   ||||||||||  |
Sbjct: 519 aatgcaaactcctgaaaatattattctttttagaggagatgatcctggatatttaggacc 578


Query: 344 agaatttcaaaacactcttcttaattcaaatggtacaattaataaa 389
            ||  |||  ||||  |||  |||||||||   |  ||||  ||||||||||||||
Sbjct: 579 ggattttgaaaatactattcttaatagagatggaacaattaataaa 624




 ☐ >gi|33149672|gb|AY330212.1|    Cloning vector pT3, complete sequence
              Length = 2551

 Score = 67.9 bits (34), Expect = 2e-08
 Identities = 41/42 (97%), Gaps = 1/42 (2%)
 Strand = Plus / Minus


Query: 1    ggatcctctagagtcgacctgcaggcatgcaatgcttattcc 42
            |||||||||||||||||||||||||||||||||||| |||||||||
Sbjct: 227  ggatcctctagagtcgacctgcaggcatgcaa-gcttattcc 187




 ☐ >gi|595779|gb|U13871.1|XXU13871    pT7T3D cloning vector, complete sequence
              Length = 2907

 Score = 67.9 bits (34), Expect = 2e-08
 Identities = 41/42 (97%), Gaps = 1/42 (2%)
 Strand = Plus / Minus


Query: 1    ggatcctctagagtcgacctgcaggcatgcaatgcttattcc 42
            |||||||||||||||||||||||||||||||||||| |||||||||
Sbjct: 230  ggatcctctagagtcgacctgcaggcatgcaa-gcttattcc 190
```

>gi|595774|gb|U13869.1|XXU13869   pT7T318U cloning vector, complete sequence
           Length = 2883

 Score = 67.9 bits (34), Expect = 2e-08
 Identities = 41/42 (97%), Gaps = 1/42 (2%)
 Strand = Plus / Minus

Query: 1   ggatcctctagagtcgacctgcaggcatgcaatgcttattcc 42
            |||||||||||||||||||||||||||||||||| |||||||||
Sbjct: 230 ggatcctctagagtcgacctgcaggcatgcaa-gcttattcc 190

>gi|1149706|emb|X86491.1|CPSPOOA   C.perfringens spoOA gene
           Length = 350

 Score = 65.9 bits (33), Expect = 9e-08
 Identities = 36/37 (97%)
 Strand = Plus / Plus

Query: 1   ggatcctctagagtcgacctgcaggcatgcaatgctt 37
            ||||||||||||||||||||||||||||||||| ||||
Sbjct: 275 ggatcctctagagtcgacctgcaggcatgcaaggctt 311

>gi|31335236|gb|AY292466.1| BAC cloning vector pBACVM4, complete sequence
           Length = 9077

 Score = 63.9 bits (32), Expect = 3e-07
 Identities = 32/32 (100%)
 Strand = Plus / Plus

Query: 1   ggatcctctagagtcgacctgcaggcatgcaa 32
            ||||||||||||||||||||||||||||||||
Sbjct: 1813 ggatcctctagagtcgacctgcaggcatgcaa 1844

>gi|30424554|gb|AY182782.1| Shuttle vector pSK5640, complete sequence
           Length = 6152

 Score = 63.9 bits (32), Expect = 3e-07
 Identities = 32/32 (100%)
 Strand = Plus / Minus

Query: 1   ggatcctctagagtcgacctgcaggcatgcaa 32
            ||||||||||||||||||||||||||||||||
Sbjct: 36   ggatcctctagagtcgacctgcaggcatgcaa 5